DT05 Rec'd PCT/PTO 0 7 OCT 2004

SEQUENCE LISTING

<110>	Terrett,	Jonathan	Α

<120> Protein Involved in Cancer

<130> 2543-1-038PCT/US

<140> PCT/GB2003/001589

<141> 2003-04-11

<150> GB0208332.7

<151> 2002-04-11

<150> GB0229875.0

<151> 2002-12-21

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 1212

<212> PRT

<213> Homo sapiens

<400> 1

Met Glu Pro Arg Pro Thr Ala Pro Ser Ser Gly Ala Pro Gly Leu Ala 1 5 10 15

Gly Val Gly Glu Thr Pro Ser Ala Ala Ala Leu Ala Ala Ala Arg Val 20 25 30

Glu Leu Pro Gly Thr Ala Val Pro Ser Val Pro Glu Asp Ala Ala Pro 35 40 45

Ala Ser Arg Asp Gly Gly Val Arg Asp Glu Gly Pro Ala Ala Ala 50 55 60

Gly Asp Gly Leu Gly Arg Pro Leu Gly Pro Thr Pro Ser Gln Ser Arg
65 70 75 80

Phe Gln Val Asp Leu Val Ser Glu Asn Ala Gly Arg Ala Ala Ala Ala 85 90 95

Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Ala Gly 100 105 110

Ala Lys Gln Thr Pro Ala Asp Gly Glu Ala Ser Gly Glu Ser Glu Pro Ala Lys Gly Ser Glu Glu Ala Lys Gly Arg Phe Arg Val Asn Phe Val Asp Pro Ala Ala Ser Ser Ser Ala Glu Asp Ser Leu Ser Asp Ala Ala Gly Val Gly Val Asp Gly Pro Asn Val Ser Phe Gln Asn Gly Gly Asp Thr Val Leu Ser Glu Gly Ser Ser Leu His Ser Gly Gly Gly Gly Ser Gly His His Gln His Tyr Tyr Tyr Asp Thr His Thr Asn Thr Tyr Tyr Leu Arg Thr Phe Gly His Asn Thr Met Asp Ala Val Pro Arg Ile Asp His Tyr Arg His Thr Ala Ala Gln Leu Gly Glu Lys Leu Leu Arg Pro Ser Leu Ala Glu Leu His Asp Glu Leu Glu Lys Glu Pro Phe Glu Asp Gly Phe Ala Asn Gly Glu Glu Ser Thr Pro Thr Arg Asp Ala Val Val Thr Tyr Thr Ala Glu Ser Lys Gly Val Val Lys Phe Gly Trp Ile Lys Gly Val Leu Val Arg Cys Met Leu Asn Ile Trp Gly Val Met Leu Phe Ile Arg Leu Ser Trp Ile Val Gly Gln Ala Gly Ile Gly Leu Ser Val Leu Val Ile Met Met Ala Thr Val Val Thr Thr Ile Thr Gly Leu Ser Thr Ser Ala Ile Ala Thr Asn Gly Phe Val Arg Gly Gly Ala Tyr Tyr Leu Ile Ser Arg Ser Leu Gly Pro Glu Phe Gly Gly Ala Ile

Gly Leu Ile Phe Ala Phe Ala Asn Ala Val Ala Val Ala Met Tyr Val Val Gly Phe Ala Glu Thr Val Val Glu Leu Leu Lys Glu His Ser Ile Leu Met Ile Asp Glu Ile Asp Ile Arg Ile Ile Gly Ala Ile Thr Val Val Ile Leu Leu Gly Ile Ser Val Ala Gly Met Glu Trp Glu Ala Lys Ala Gln Ile Val Leu Leu Val Ile Leu Leu Ala Ile Gly Asp Phe Val Ile Gly Thr Phe Ile Pro Leu Glu Ser Lys Lys Pro Lys Gly Phe Phe Gly Tyr Lys Ser Glu Ile Phe Asn Glu Asn Phe Gly Pro Asp Phe Arg Glu Glu Thr Phe Phe Ser Val Phe Ala Ile Phe Phe Pro Ala Ala Thr Gly Ile Leu Ala Gly Ala Asn Ile Ser Gly Asp Leu Ala Asp Pro Gln Ser Ala Ile Pro Lys Gly Thr Leu Leu Ala Ile Leu Ile Thr Thr Leu Val Tyr Val Gly Ile Ala Val Ser Val Gly Ser Cys Val Val Arg Asp Ala Thr Gly Asn Val Asn Asp Thr Ile Val Thr Glu Leu Thr Asn Cys Thr Ser Ala Ala Cys Lys Leu Asn Phe Asp Phe Ser Ser Cys Glu Ser Ser Pro Cys Ser Tyr Gly Leu Met Asn Asn Phe Gln Val Met Ser Met Val Ser Gly Phe Thr Pro Leu Ile Ser Ala Gly Ile Phe Ser Ala Thr Leu Ser Ser Ala Leu Ala Ser Leu Val Ser Ala Pro Lys

Ile Phe Gln Ala Leu Cys Lys Asp Asn Ile Tyr Pro Ala Phe Gln Met Phe Ala Lys Gly Tyr Gly Lys Asn Asn Glu Pro Leu Arg Gly Tyr Ile Leu Thr Phe Leu Ile Ala Leu Gly Phe Ile Leu Ile Ala Glu Leu Asn Val Ile Ala Pro Ile Ile Ser Asn Phe Phe Leu Ala Ser Tyr Ala Leu Ile Asn Phe Ser Val Phe His Ala Ser Leu Ala Lys Ser Pro Gly Trp Arg Pro Ala Phe Lys Tyr Tyr Asn Met Trp Ile Ser Leu Leu Gly Ala Ile Leu Cys Cys Ile Val Met Phe Val Ile Asn Trp Trp Ala Ala Leu Leu Thr Tyr Val Ile Val Leu Gly Leu Tyr Ile Tyr Val Thr Tyr Lys Lys Pro Asp Val Asn Trp Gly Ser Ser Thr Gln Ala Leu Thr Tyr Leu Asn Ala Leu Gln His Ser Ile Arg Leu Ser Gly Val Glu Asp His Val Lys Asn Phe Arg Pro Gln Cys Leu Val Met Thr Gly Ala Pro Asn Ser Arg Pro Ala Leu Leu His Leu Val His Asp Phe Thr Lys Asn Val Gly Leu Met Ile Cys Gly His Val His Met Gly Pro Arg Arg Gln Ala Met Lys Glu Met Ser Ile Asp Gln Ala Lys Tyr Gln Arg Trp Leu Ile Lys Asn Lys Met Lys Ala Phe Tyr Ala Pro Val His Ala Asp Asp Leu Arg Glu Gly Ala Gln Tyr Leu Met Gln Ala Ala Gly Leu Gly Arg Met Lys

- Pro Asn Thr Leu Val Leu Gly Phe Lys Lys Asp Trp Leu Gln Ala Asp 885 890 895
- Met Arg Asp Val Asp Met Tyr Ile Asn Leu Phe His Asp Ala Phe Asp 900 905 910
- Ile Gln Tyr Gly Val Val Val Ile Arg Leu Lys Glu Gly Leu Asp Ile 915 920 925
- Ser His Leu Gln Gly Gln Glu Leu Leu Ser Ser Gln Glu Lys Ser 930 935 940
- Pro Gly Thr Lys Asp Val Val Val Ser Val Glu Tyr Ser Lys Lys Ser 945 950 955 960
- Asp Leu Asp Thr Ser Lys Pro Leu Ser Glu Lys Pro Ile Thr His Lys 965 970 975
- Val Glu Glu Asp Gly Lys Thr Ala Thr Gln Pro Leu Leu Lys Lys 980 985 990
- Glu Ser Lys Gly Pro Ile Val Pro Leu Asn Val Ala Asp Gln Lys Leu 995 1000 1005
- Leu Glu Ala Ser Thr Gln Phe Gln Lys Lys Gln Gly Lys Asn Thr 1010 1015 1020
- Ile Asp Val Trp Trp Leu Phe Asp Asp Gly Gly Leu Thr Leu Leu 1025 1030 1035
- Ile Pro Tyr Leu Leu Thr Thr Lys Lys Lys Trp Lys Asp Cys Lys 1040 1045 1050
- Ile Arg Val Phe Ile Gly Gly Lys Ile Asn Arg Ile Asp His Asp 1055 1060 1065
- Arg Arg Ala Met Ala Thr Leu Leu Ser Lys Phe Arg Ile Asp Phe 1070 1075 1080
- Ser Asp Ile Met Val Leu Gly Asp Ile Asn Thr Lys Pro Lys Lys 1085 1090 1095
- Glu Asn Ile Ile Ala Phe Glu Glu Ile Ile Glu Pro Tyr Arg Leu 1100 1105 1110
- His Glu Asp Asp Lys Glu Gln Asp Ile Ala Asp Lys Met Lys Glu 1115 1120 1125

- Asp Glu Pro Trp Arg Ile Thr Asp Asn Glu Leu Glu Leu Tyr Lys 1130 1135 1140
- Thr Lys Thr Tyr Arg Gln Ile Arg Leu Asn Glu Leu Leu Lys Glu
 1145 1150 1155
- His Ser Ser Thr Ala Asn Ile Ile Val Met Ser Leu Pro Val Ala 1160 1165 1170
- Arg Lys Gly Ala Val Ser Ser Ala Leu Tyr Met Ala Trp Leu Glu 1175 1180 1185
- Ala Leu Ser Lys Asp Leu Pro Pro Ile Leu Leu Val Arg Gly Asn 1190 1195 1200
- His Gln Ser Val Leu Thr Phe Tyr Ser 1205 1210
- <210> 2
- <211> 4098
- <212> DNA
- <213> Homo sapiens
- 1<400> 2
- ggtggcctct gtggccgtcc aggctagcgg cggcccgcag gcggcgggga gaaagactct 60
- ctcacctggt cttgcggctg tggccaccgc cggccagggg tgtggagggc gtgctgccgg 120
- agacgtccgc cgggctctgc agttccgccg ggggtcgggc agctatggag ccgcggccca 180
- cggcgccctc ctccggcgcc ccgggactgg ccggggtcgg ggagacgccg tcagccgctg 240
- cgctggccgc agccagggtg gaactgcccg gcacggctgt gccctcggtg ccggaggatg 300
- ctgcgcccgc gagccgggac ggcgggggg tccgcgatga gggccccgcg gcggccgggg 360
- acgggctggg cagacccttg gggcccaccc cgagccagag ccgtttccag gtggacctgg 420
- tttccgagaa cgccggggg gccgctgctg cggcggcggc ggcggcggcg gcagcggcgg 480

- cggctggtgc tggggcgggg gccaagcaga cccccgcgga cggggaagcc agcggcgaga 540
- gcgagccagc taaaggcagc gaggaagcca agggccgctt ccgcgtgaac ttcgtggacc 600
- cagctgcctc ctcgtcggct gaagacagcc tgtcagatgc tgccggggtc ggagtcgacg 660
- ggcccaacgt gagcttccag aacggcgggg acacggtgct gagcgagggc agcagcctgc 720
- actccggcgg cggcggcgc agtgggcacc accagcacta ctattatgat acccacacca 780
- acacctacta cctgcgcacc ttcggccaca acaccatgga cgctgtgccc aggatcgatc 840
- actaccggca cacagccgcg cagctgggcg agaagctgct ccggcctagc ctggcggagc 900
- tccacgacga gctggaaaag gaaccttttg aggatggctt tgcaaatggg gaagaaagta 960
- ctccaaccag agatgctgtg gtcacgtata ctgcagaaag taaaggagtc gtgaagtttg 1020
- gctggatcaa gggtgtatta gtacgttgta tgttaaacat ttggggtgtg atgcttttca 1080
- ttagattgtc atggattgtg ggtcaagctg gaataggtct atcagtcctt gtaataatga 1140
- tggccactgt tgtgacaact atcacaggat tgtctacttc agcaatagca actaatggat 1200
- ttgtaagagg aggaggagca tattatttaa tatctagaag tctagggcca gaatttggtg 1260
- gtgcaattgg tctaatcttc gcctttgcca acgctgttgc agttgctatg tatgtggttg 1320
- gatttgcaga aaccgtggtg gagttgctta aggaacattc catacttatg atagatgaaa 1380
- tcaatgatat ccgaattatt ggagccatta cagtcgtgat tcttttaggt atctcagtag 1440

- ctggaatgga gtgggaagca aaagctcaga ttgttctttt ggtgatccta cttcttgcta 1500
- ttggtgattt cgtcatagga acatttatcc cactggagag caagaagcca aaagggtttt 1560
- ttggttataa atctgaaata tttaatgaga actttgggcc cgattttcga gaggaagaga 1620
- ctttctttc tgtatttgcc atctttttc ctgctgcaac tggtattctg gctggagcaa 1680
- atatctcagg tgatcttgca gatcctcagt cagccatacc caaaggaaca ctcctagcca 1740
- ttttaattac tacattggtt tacgtaggaa ttgcagtatc tgtaggttct tgtgttgttc 1800
- gagatgccac tggaaacgtt aatgacacta tcgtaacaga gctaacaaac tgtacttctg 1860
- cagcctgcaa attaaacttt gatttttcat cttgtgaaag cagtccttgt tcctatggcc 1920
- taatgaacaa cttccaggta atgagtatgg tgtcaggatt tacaccacta atttctgcag 1980
- gtatattttc agccactctt tcttcagcat tagcatccct agtgagtgct cccaaaatat 2040
- ttcaggctct atgtaaggac aacatctacc cagctttcca gatgtttgct aaaggttatg 2100
- ggaaaaataa tgaacctctt cgtggctaca tcttaacatt cttaattgca cttggattca 2160
- tcttaattgc tgaactgaat gttattgcac caattatctc aaacttcttc cttgcatcat 2220
- atgcattgat caatttttca gtattccatg catcacttgc aaaatctcca ggatggcgtc 2280
- ctgcattcaa atactacaac atgtggatat cacttcttgg agcaattctt tgttgcatag 2340
- taatgttcgt cattaactgg tgggctgcat tgctaacata tgtgatagtc cttgggctgt 2400

- atatttatgt tacctacaaa aaaccagatg tgaattgggg atcctctaca caagccctga 2460
- cttacctgaa tgcactgcag cattcaattc gtctttctgg agtggaagac cacgtgaaaa 2520
- actttaggcc acagtgtctt gttatgacag gtgctccaaa ctcacgtcca gctttacttc 2580
- atcttgttca tgatttcaca aaaaatgttg gtttgatgat ctgtggccat gtacatatgg 2640
- gtcctcgaag acaagccatg aaagagatgt ccatcgatca agccaaatat cagcgatggc 2700
- ttattaagaa caaaatgaag gcattttatg ctccagtaca tgcagatgac ttgagagaag 2760 .
- gtgcacagta tttgatgcag gctgctggtc ttggtcgtat gaagccaaac acacttgtcc 2820
- ttggatttaa gaaagattgg ttgcaagcag atatgaggga tgtggatatg tatataaact 2880
- tatttcatga tgcttttgac atacaatatg gagtagtggt tattcgccta aaagaaggtc 2940
- tggatatatc tcatcttcaa ggacaagaag aattattgtc atcacaagag aaatctcctg 3000
- gcaccaagga tgtggtagta agtgtggaat atagtaaaaa gtccgattta gatacttcca 3060
- aaccactcag tgaaaaacca attacacaca aagttgagga agaggatggc aagactgcaa 3120
- ctcaaccact gttgaaaaaa gaatccaaag gccctattgt gcctttaaat gtagctgacc 3180
- aaaagcttct tgaagctagt acacagtttc agaaaaaaca aggaaagaat actattgatg 3240
- agaaaaaatg gaaagactgt aagatcagag tattcattgg tggaaagata aacagaatag 3360

- accatgaccg gagagcgatg gctactttgc ttagcaagtt ccggatagac ttttctgata 3420
- tcatggttct aggagatatc aataccaaac caaagaaaga aaatattata gcttttgagg 3480
- aaatcattga gccatacaga cttcatgaag atgataaaga gcaagatatt gcagataaaa 3540
- tgaaagaaga tgaaccatgg cgaataacag ataatgagct tgaactttat aagaccaaga 3600
- cataccggca gatcaggtta aatgagttat taaaggaaca ttcaagcaca gctaatatta 3660
- ttgtcatgag tctcccagtt gcacgaaaag gtgctgtgtc tagtgctctc tacatggcat 3720
- ggttagaagc tctatctaag gacctaccac caatcctcct agttcgtggg aatcatcaga 3780
- gtgtccttac cttctattca taaatgttct atacagtgga cagccctcca gaatggtact 3840
- tcagtgccta gtgtagtaac ctgaaatctt caatgacaca ttaacatcac aatggcgaat 3900
- ggtgactttt ctttcacgat ttcattaatt tgaaagcaca caggaaagct tgctccattg 3960
- ataacgtgta tggagacttc ggttttagtc aattccatat ctcaatctta atggtgattc 4020
- ttctctgttg aactgaagtt tgtgagagta gttttccttt gctacttgaa tagcaataaa 4080
- agcgtgttaa ctttttgg 4098
- <210> 3
- <211> 22
- <212> DNA
- <213> Artificial sequence
- 1<220>
- <223> Primer
- <400> 3
- cacctactac ctgcgcacct tc

```
<210> 4
<211> 22
<212> DNA
      Artificial sequence
<213>
1<220>
<223> Primer
<400> 4
gaccacagca tctctggttg ga
   22
<210>
       5
<211> 12
<212> PRT
<213> Artificial sequence
1<220>
<223> synthetic peptide
<400>
Ser Lys Lys Pro Lys Gly Phe Phe Gly Tyr Lys Cys
                5
<210>
       6
<211>
      16
<212>
      PRT
<213> Artificial sequence
1<220>
<223> synthetic peptide
<400>
      6
Ser Gly Glu Ser Glu Pro Ala Lys Gly Ser Glu Glu Ala Lys Gly Cys
                5
                                    10
                                                        15
1
```